

# M Azim Ansari

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

3,928  
citations

236833

25  
h-index

155592

55  
g-index

86  
all docs

86  
docs citations

86  
times ranked

8864  
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. <i>Nature Immunology</i> , 2020, 21, 1336-1345.	7.0	1,066
2	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
3	Immunogenicity of standard and extended dosing intervals of BNT162b2 mRNA vaccine. <i>Cell</i> , 2021, 184, 5699-5714.e11.	13.5	262
4	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	13.9	199
5	Safety and immunogenicity of the ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 in HIV infection: a single-arm substudy of a phase 2/3 clinical trial. <i>Lancet HIV</i> , 2021, 8, e474-e485.	2.1	190
6	T-cell and antibody responses to first BNT162b2 vaccine dose in previously infected and SARS-CoV-2-naïve UK health-care workers: a multicentre prospective cohort study. <i>Lancet Microbe</i> , 2022, 3, e21-e31.	3.4	131
7	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	9.4	129
8	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	1.8	112
9	T cell assays differentiate clinical and subclinical SARS-CoV-2 infections from cross-reactive antiviral responses. <i>Nature Communications</i> , 2021, 12, 2055.	5.8	102
10	Recombinational Switching of the <i>Clostridium difficile</i> S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2013, 207, 675-686.	1.9	93
11	Insights From Deep Sequencing of the HBV Genome—Unique, Tiny, and Misunderstood. <i>Gastroenterology</i> , 2019, 156, 384-399.	0.6	92
12	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	5.1	82
13	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	1.6	75
14	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019, 69, 1861-1872.	3.6	68
15	ve-SEQ: Robust, unbiased enrichment for streamlined detection and whole-genome sequencing of HCV and other highly diverse pathogens. <i>F1000Research</i> , 2015, 4, 1062.	0.8	66
16	Efficient Inference of Recombination Hot Regions in Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1593-1605.	3.5	62
17	Evolutionary dynamics of <i>Enterococcus faecium</i> reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016, 2, .	1.0	50
18	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016, 22, 671-678.	2.0	46

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19	Inference of the Properties of the Recombination Process from Whole Bacterial Genomes. <i>Genetics</i> , 2014, 196, 253-265.	1.2	41
20	Bayesian Inference of the Evolution of a Phenotype Distribution on a Phylogenetic Tree. <i>Genetics</i> , 2016, 204, 89-98.	1.2	40
21	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	39
22	Analysis of genomic-length HBV sequences to determine genotype and subgenotype reference sequences. <i>Journal of General Virology</i> , 2020, 101, 271-283.	1.3	38
23	Highly-Immunogenic Vially-Vectored T-cell Vaccines Cannot Overcome Subversion of the T-cell Response by HCV during Chronic Infection. <i>Vaccines</i> , 2016, 4, 27.	2.1	35
24	Extensive C->U transition biases in the genomes of a wide range of mammalian RNA viruses; potential associations with transcriptional mutations, damage- or host-mediated editing of viral RNA. <i>PLoS Pathogens</i> , 2021, 17, e1009596.	2.1	32
25	Role of HIV-specific CD8+ T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , 2017, 214, 3239-3261.	4.2	31
26	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	1.5	29
27	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	2.8	28
28	Amino Acid Substitutions in Genotype 3a Hepatitis C Virus Polymerase Protein Affect Responses to Sofosbuvir. <i>Gastroenterology</i> , 2019, 157, 692-704.e9.	0.6	27
29	Durability of ChAdOx1 nCoV-19 vaccination in people living with HIV. <i>JCI Insight</i> , 2022, 7, .	2.3	26
30	Electronic Health Informatics Data To Describe Clearance Dynamics of Hepatitis B Surface Antigen (HBsAg) and e Antigen (HBeAg) in Chronic Hepatitis B Virus Infection. <i>MBio</i> , 2019, 10, .	1.8	24
31	Risk of Reactivation of Hepatitis B Virus (HBV) and Tuberculosis (TB) and Complications of Hepatitis C Virus (HCV) Following Tocilizumab Therapy: A Systematic Review to Inform Risk Assessment in the COVID-19 Era. <i>Frontiers in Medicine</i> , 2021, 8, 706482.	1.2	23
32	Strong sex bias in elite control of paediatric HIV infection. <i>Aids</i> , 2019, 33, 67-75.	1.0	22
33	The Design and Development of a Multi-HBV Antigen Encoded in Chimpanzee Adenoviral and Modified Vaccinia Ankara Viral Vectors; A Novel Therapeutic Vaccine Strategy against HBV. <i>Vaccines</i> , 2020, 8, 184.	2.1	21
34	Divergent trajectories of antiviral memory after SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, 1251.	5.8	20
35	Genetic variation in <i>TERT</i> modifies the risk of hepatocellular carcinoma in alcohol-related cirrhosis: results from a genome-wide case-control study. <i>Gut</i> , 2023, 72, 381-391.	6.1	19
36	Impact of Interferon Lambda 4 Genotype on Interferon- $\alpha$ -Stimulated Gene Expression During Direct-Acting Antiviral Therapy for Hepatitis C. <i>Hepatology</i> , 2018, 68, 859-871.	3.6	18

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37	Evidence of CD4+ T cell-mediated immune pressure on the Hepatitis C virus genome. <i>Scientific Reports</i> , 2018, 8, 7224.	1.6	16
38	Testing for dependence on tree structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9787-9792.	3.3	16
39	Real world SOF/VEL/VOX retreatment outcomes and viral resistance analysis for HCV patients with prior failure to DAA therapy. <i>Journal of Viral Hepatitis</i> , 2021, 28, 1256-1264.	1.0	16
40	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	5.8	16
41	HBV vaccination and PMTCT as elimination tools in the presence of HIV: insights from a clinical cohort and dynamic model. <i>BMC Medicine</i> , 2019, 17, 43.	2.3	15
42	Technical Validation of a Hepatitis C Virus Whole Genome Sequencing Assay for Detection of Genotype and Antiviral Resistance in the Clinical Pathway. <i>Frontiers in Microbiology</i> , 2020, 11, 576572.	1.5	13
43	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. <i>Scientific Reports</i> , 2020, 10, 9838.	1.6	13
44	Interferon lambda 4 variant rs12979860 is not associated with RAV NS5A Y93H in hepatitis C virus genotype 3a. <i>Hepatology</i> , 2016, 64, 1377-1378.	3.6	12
45	Global prevalence and phylogeny of hepatitis B virus (HBV) drug and vaccine resistance mutations. <i>Journal of Viral Hepatitis</i> , 2021, 28, 1110-1120.	1.0	12
46	An HLA-I signature favouring KIR-educated Natural Killer cells mediates immune control of HIV in children and contrasts with the HLA-B-restricted CD8+ T-cell-mediated immune control in adults. <i>PLoS Pathogens</i> , 2021, 17, e1010090.	2.1	12
47	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020, 222, S666-S671.	1.9	11
48	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021, 12, 6105.	5.8	11
49	Performance of models to predict hepatocellular carcinoma risk among UK patients with cirrhosis and cured HCV infection. <i>JHEP Reports</i> , 2021, 3, 100384.	2.6	10
50	The rs429358 Locus in Apolipoprotein E Is Associated With Hepatocellular Carcinoma in Patients With Cirrhosis. <i>Hepatology Communications</i> , 2022, 6, 1213-1226.	2.0	9
51	Impact of virus subtype and host IFNL4 genotype on large-scale RNA structure formation in the genome of hepatitis C virus. <i>Rna</i> , 2020, 26, 1541-1556.	1.6	7
52	Safety and Immunogenicity of the ChAdox1 nCoV-19 (AZD1222) Vaccine Against SARS-CoV-2 in HIV Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	6
53	High Cure Rates for Hepatitis C Virus Genotype 6 in Advanced Liver Fibrosis With 12 Weeks Sofosbuvir and Daclatasvir: The Vietnam SEARCH Study. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab267.	0.4	6
54	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	0.9	3

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55	Defining the key intrahepatic gene networks in HCV infection driven by sex. <i>Gut</i> , 2023, 72, 984-994.	6.1	3
56	In vivo negative regulation of SARS-CoV-2 receptor, ACE2, by interferons and its genetic control. <i>Wellcome Open Research</i> , 0, 6, 47.	0.9	2
57	Endemic HBV among hospital in-patients in Bangladesh, including evidence of occult infection. <i>Journal of General Virology</i> , 2021, 102, .	1.3	2
58	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	0.9	2
59	Genome-To-Genome Virus-Host Analysis Reveals HCV Genotype 3 Viral Polymorphisms Linked Viral Load and to Host HLA Class-I/II and IL28B Alleles. <i>Journal of Hepatology</i> , 2016, 64, S419.	1.8	1
60	SAT-182-Full length deep sequencing of South African hepatitis B virus isolates reveals increased viral diversity and X-gene deletions in hepatocellular carcinoma patients. <i>Journal of Hepatology</i> , 2019, 70, e709-e710.	1.8	0
61	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021, 7, veab065.	2.2	0
62	Variable short duration treatment versus standard treatment, with and without adjunctive ribavirin, for chronic hepatitis C: the STOP-HCV-1 non-inferiority, factorial RCT. <i>Efficacy and Mechanism Evaluation</i> , 2021, 8, 1-90.	0.9	0